AMENDMENTS TO THE CLAIMS

1. **(Previously presented)** A screening and/or quantification method of one or more transcriptional factors(s) present in a cell or cell lysate, said method comprising the steps of:

a. binding to an insoluble solid support double-stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm^2 of said solid support surface, wherein the solid support is an array bearing at least 4 spots/cm^2 of solid support surface, each spot containing double-stranded DNA sequence(s) for the binding of transcriptional factor(s), said double-stranded DNA sequence comprising a specific sequence, said specific sequence being able to bind said one or more transcriptional factor(s) and said double-stranded DNA sequence being connected to the surface of the solid support by a spacer corresponding to or comprising at least a double-stranded DNA nucleotide sequence of between about 50 and about 250 base pairs;

b. putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequence(s); and

c. identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s).

2. **(Original)** The method according to claim 1, wherein the transcriptional factor is present in solution at concentration lower than 20 nmolar (nM).

3. **(Canceled)**

4. **(Original)** The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is a non-radioactive resulting signal.

5. **(Previously presented)** The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is obtained through an enzymatic reaction.

6. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors present in a same biological sample.

7. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of transcriptional factors selected from the group consisting of NF-KB, AP-1, CREB, SP-1, C/EBP, GR, HIF-1, Myc, NF-AT, Oct, TBP, CBF-1 and factors listed in table 1.

8. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors upon a same support upon the same multiwell plate.

9.-11. **(Cancelled)**

12. **(Previously presented)** The method according to claim 1, wherein the binding of the double-stranded DNA sequence(s) to the insoluble solid support is of non-covalent type and includes a binding pair comprising a first member and a second member, said first member being bound to the double-stranded DNA sequence, said second member being bound to the surface of the solid support.

13. **(Original)** The method according to claim 1, wherein the double-stranded DNA sequence(s) are covalently bound to the surface of the insoluble solid support.

14. **(Currently amended)** The method according to claim 1, wherein the ~~consensus~~ specific sequence is repeated on the same molecule.

15. **(Currently amended)** The method according to claim 1, wherein the double-stranded DNA sequences fixed on the support surface contain in part or totally one or several of the ~~consensus~~ specific DNA sequences presented in the table 1.

16. **(Currently amended)** ~~The method according to claim 1~~ A screening and/or quantification method of one or more transcriptional factors(s) present in a cell or cell lysate, said method comprising the steps of:

a. binding to an insoluble solid support double-stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm^2 of said solid support surface, wherein the solid support is an array bearing at least 4 spots/cm^2 of solid support surface, each spot containing double-stranded DNA sequence(s) for the binding of transcriptional factor(s), said double-stranded DNA sequence comprising a specific sequence, said specific sequence being able to bind said one or more transcriptional factor(s) and said double-stranded DNA sequence being connected to the surface of the solid support by a spacer corresponding to or comprising at least a double-stranded DNA nucleotide sequence of between about 50 and about 250 base pairs;

b. putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequence(s); and

c. identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s),

wherein said transcriptional factor is the HIV integrase.

17. **(Original)** The method according to claim 1, comprising the step of identification of at least one characteristic specific of the transcriptional factor activation.

18. **(Original)** The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds able to bind to said transcriptional factor(s) or inhibit the binding of transcriptional factor(s) to the specific sequence upon the double-stranded DNA sequence(s) bound to said solid support.

19. **(Original)** The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds which modulate the binding and/or the activity of the said transcriptional factor(s) when they are put in contact with cells, tissues or organisms.

20. **(Original)** The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds which modulate the activity of enzyme(s) or protein(s) acting on transcriptional factor(s) and then assayed for the binding to and/or activity of said transcriptional factor(s).

21. **(Original)** A method according to claim 1, which comprises the step of identification of transcriptional factor(s) and/or of peptides which are part of their active complex.

22. **(Original)** The method according to claim 1, which comprises the step of adding in the cell lysate an externally added transcriptional factor or a compound which is able to bind to the consensus sequence.

23.-33. **(Cancelled)**

34. **(Currently amended)** The method of Claim 12 ~~36~~, wherein said binding pair is biotin/streptavidin.

35. **(Cancelled)**

36. **(Previously presented)** The method according to claim 12, wherein the binding pair is selected from the group consisting of biotin/streptavidin, hapten/receptor and antigen/antibody binding pair.

37. **(Previously presented)** The method according to claim 1, wherein step b) comprises putting into contact said one or more transcriptional factor(s) in a cell lysate with said bound double-stranded DNA sequence(s).

38. **(Cancelled)**